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============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2010; month=2; day=1; hr=13; min=2; sec=58; ms=699; ]
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Application No: 10552013   Version No: 4.0

Input Set:

Output Set:

Started:	2010-01-18 15:26:47.295
Finished:	2010-01-18 15:26:57.833
Elapsed:	0 hr(s) 0 min(s) 10 sec(s) 538 ms
Total Warnings:	103
Total Errors:	51
No. of SeqIDs Defined:	148
Actual SeqID Count:	148

Error code		Error Description
W	402	Undefined organism found in <213> in SEQ ID (1)
W	402	Undefined organism found in <213> in SEQ ID (2)
W	402	Undefined organism found in <213> in SEQ ID (16)
W	402	Undefined organism found in <213> in SEQ ID (17)
W	402	Undefined organism found in <213> in SEQ ID (18)
W	402	Undefined organism found in <213> in SEQ ID (19)
W	402	Undefined organism found in <213> in SEQ ID (28)
W	402	Undefined organism found in <213> in SEQ ID (29)
W	402	Undefined organism found in <213> in SEQ ID (30)
W	402	Undefined organism found in <213> in SEQ ID (31)
W	402	Undefined organism found in <213> in SEQ ID (32)
W	402	Undefined organism found in <213> in SEQ ID (33)
W	402	Undefined organism found in <213> in SEQ ID (36)
W	402	Undefined organism found in <213> in SEQ ID (37)
W	213	Artificial or Unknown found in <213> in SEQ ID (52)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W	213	Artificial or Unknown found in <213> in SEQ ID (53)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W	213	Artificial or Unknown found in <213> in SEQ ID (54)

Input Set:

                Output Set:

                    Started: 2010-01-18 15:26:47.295
                   Finished: 2010-01-18 15:26:57.833
                    Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 538 ms
            Total Warnings: 103
              Total Errors: 51
      No. of SeqIDs Defined: 148
          Actual SeqID Count: 148

Error code   Error Description

E   224   <220>,<223> section required as <213> has Artificial sequence or
                 Unknown in SEQID (54)

W   213   Artificial or Unknown found in <213> in SEQ ID (55)

E   224   <220>,<223> section required as <213> has Artificial sequence or
                 Unknown in SEQID (55)

W   213   Artificial or Unknown found in <213> in SEQ ID (56)

W   213   Artificial or Unknown found in <213> in SEQ ID (60)

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W   213   Artificial or Unknown found in <213> in SEQ ID (62)

W   213   Artificial or Unknown found in <213> in SEQ ID (63)

W   213   Artificial or Unknown found in <213> in SEQ ID (64)

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W   213   Artificial or Unknown found in <213> in SEQ ID (71)

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W   213   Artificial or Unknown found in <213> in SEQ ID (76)

E   224   <220>,<223> section required as <213> has Artificial sequence or
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W   213   Artificial or Unknown found in <213> in SEQ ID (77)

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            Input Set:


            Output Set:



             Started:   2010-01-18 15:26:47.295
            Finished:   2010-01-18 15:26:57.833
             Elapsed:   0 hr(s) 0 min(s) 10 sec(s) 538 ms
     Total Warnings:    103
       Total Errors:    51
No. of SeqIDs Defined:  148
  Actual SeqID Count:   148
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Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79) This error has occured more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
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SEQUENCE LISTING

<110> Renz, Andreas
       Sozer, Nursen
       Frentzen, Margit
       Bauer, Jorg
       Keith, Stobart
       Fraser, Thomas
       Lazarus, Colin M
       Qi, Baoxiu
       Abbadi, Amine
       Heinz, Ernst

<120> NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
       UNSATURATED FATTY ACIDS

<130> 13478-00002-US

<140> 10552013
<141> 2005-09-30

<150> PCT/EP2004/003224
<151> 2004-03-26

<150> DE103 14 759.4
<151> 2003-03-31

<150> DE103 48 996.7
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<160> 148

<170> PatentIn version 3.3

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<213> Thraustochytrium

<220>
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<222> (38)..(952)
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Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
          10   15   20
ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc   151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
          25   30   35
acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc   199
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys

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gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc      247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
55                      60                      65                      70
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg      295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
                    75                      80                      85
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac      343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
                        90                      95                     100
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc      391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
            105                     110                     115
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc      439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
            120                     125                     130
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct      487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
135                     140                     145                     150
cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg      535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
                    155                     160                     165
ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag      583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
                    170                     175                     180
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag      631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
            185                     190                     195
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg      679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
        200                     205                     210
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac      727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
215                     220                     225                     230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag      775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
                    235                     240                     245
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg      823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
                    250                     255                     260
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc      871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
            265                     270                     275
gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga      919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
        280                     285                     290
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca   972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
295                     300                     305
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<212>   PRT
<213>   Thraustochytrium
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Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
        35   40   45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
    50   55   60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65   70   75   80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
            85   90   95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
            100   105   110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
        115   120   125
Ile Val Asp Arg Glu Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
    130   135   140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145   150   155   160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
                165   170   175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
            180   185   190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
        195   200   205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
210   215   220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225   230   235   240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
                245   250   255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
            260   265   270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
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Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
    290   295   300
Leu
305

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<213>   Physcomitrella patens

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aactgaaaac ttgttttaat tttttcttaa attgaaattc tgtgcctgaa agccaactct   180

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aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct      240
tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg      300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag      360
ggatatggat gttgtaaagg tgattttttgc aggtgataaa gtacctaagg agaaccgtgt      420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat      480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc      540
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gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtaccc atccatggct      720
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gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact      960
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aagctttatg tggctttcgc tagtttgctg ctcgcgttta gtacctattt tgattggaga     1380
cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt     1440
agttgtaatt ggtttgttta ttccgattcc aaagctgagt ttaagggtga ggctcctctt     1500
taagctgatt tttgctatta attggctgct cccttgtttg tctgccgtaa attggcttta     1560
atacggttgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt     1620
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<223> LPAAT

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1               5                   10                  15

tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc       96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                  30

aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat      144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                  40                  45

gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa      192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                  55                  60

ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt      240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80

gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac      288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85                  90                  95
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            100                 105                 110
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca      384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
            115                 120                 125
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat      432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
        130                 135                 140
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca      480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg      528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
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gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta      576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
            180                 185                 190
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Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
            195                 200                 205
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa      672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
        210                 215                 220
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Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                 230                 235


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<212>   PRT
<213>   Physcomitrella patens

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1               5                   10                  15
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            20                  25                  30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                  40                  45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                  55                  60
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85                  90                  95
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
            100                 105                 110
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
            115                 120                 125
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
        130                 135                 140
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                 170                 175
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
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```
                  180                   185                   190
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
        195                   200                   205
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
    210                   215                   220
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                   230                   235


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<212>   DNA
<213>   Physcomitrella patens

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<221>   misc_feature
<223>   LPAAT

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acaatatgtg tcccacgtc atgttgttcc cggagggcac taccaccaat ggcagagcaa      180
taatcgcctt caaaacagga gcattttcgc ctggtctccc tgtgcagcca atggttatta     240
gataccctca caagtatgtc aacccctctt ggtgtgacca aggaggtccg ttggtcgttg     300
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agccaactgt gagagagatg aaataccctc atgaattcgc aagtagagtt cgcagcgaga     420
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<213>   Physcomitrella patens

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<222>   (1)..(1566)
<223>   LPAAT

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1               5                   10                  15
ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa      96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
            20                  25                  30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc     144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
        35                  40                  45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg     192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
    50                  55                  60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg     240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                  70                  75                  80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc     288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
                85                  90                  95
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```
ggc gtc aca gat ccc ttg ttt aag cct ttc aat ccg tgt cga cgg ttc        336
G
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